

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 16, 2004, 07:46:14 / Search time 0.691275 Seconds
(without alignments)
0.145 Million cell updates/sec

Title: US-09-879-257A-1

Perfect score: 206
Sequence: 1 QTDMSRKAFVPPKESDTSYV.....WRALKVEVGGEVFTKPLWP 206

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1 seqs, 486 residues

Word size : 6

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : rapb6.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	ID	Description
No.	Score	Match	Length DB

No matches found

Search completed: December 16, 2004, 07:46:15
Job time : 0.691275 secs

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OM protein - protein search, using sw model

Run on: December 16, 2004, 07:47:32 ; Search time 0.001 Seconds
(without alignments)
200.232 Million cell updates/sec

Title: us-09-879-257a-1
Perfect score: 206
Sequence: 1 QTDMSRAKAFVPPKESDTSYV.....WRALKYEVQGEVFTTKPQLMP 206

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2 seqs, 972 residues

Word size : 6

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : rapm6.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description

No matches found

Search completed: December 16, 2004, 07:47:32
Job time : 0.001 secs

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OM protein - protein search, using sw model

Run on: December 16, 2004, 07:48:45 ; Search time 0.001 Seconds
(without alignments)
100.116 Million cell updates/sec

Title: US-09-879-257A-1
Perfect score: 206
Sequence: 1 QTDMSRKAFVFPKESDTSYV.....WRALKVEVGSEVFTKPLWP 206

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1 seqs, 486 residues

Word size : 6

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : rpr6.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	ID	Description
No.	Score	Match	Length DB

No matches found			

Search completed: December 16, 2004, 07:48:45
Job time : 0.001 secs

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OM protein - protein search, using sw model

Run on: December 16, 2004, 07:43:29 ; Search time 0.001 Seconds
(without alignments)
31.104 Million cell updates/sec

Title: US-09-879-257A-2

Perfect score: 16

Sequence: 1 DMSRKAFVFPKESDTS 16

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 4 seqs, 1944 residues

Word size : 6

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 45 summaries

Database : rag6.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
No matches found					

Search completed: December 16, 2004, 07:43:29
Job time : 0.001 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 16, 2004, 07:46:14 ; Search time 0.0536913 Seconds
(without alignments)
0.145 Million cell updates/sec

Title: US-09-879-257A-2

Perfect score: 16

Sequence: 1 DMSRKAFVFPKESDTS 16

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1 seqs, 486 residues

Word size : 6

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : rapb6.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description

No matches found

Search completed: December 16, 2004, 07:46:15
Job time : 0.0536913 secs

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OM protein - protein search, using sw model

Run on: December 16, 2004, 07:47:32 ; Search time 0.001 Seconds
(without alignments)
15.552 Million cell updates/sec

Title: US-09-879-257A-2
Perfect score: 16
Sequence: 1 DMSRKAFVFPKESDTS 16

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2 seqs, 972 residues

Word size : 6

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : rapm6.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query			
No.	Score	Match	Length	ID
Description				

No matches found

Search completed: December 16, 2004, 07:47:32
Job time : 0.001 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 16, 2004, 07:48:45 : Search time 0.001 Seconds
(without alignments)
7.776 Million cell updates/sec

Title: US-09-879-257A-2
Perfect score: 16
Sequence: 1 DMSRKAFVFPKESDTS 16

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1 seqs, 486 residues

Word size : 6

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : rpr6.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
No matches found					

Search completed: December 16, 2004, 07:48:45
Job time : 0.001 secs

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OM protein - protein search, using sw model

Run on: December 16, 2004, 07:43:29 ; Search time 0.001 Seconds
(without alignments)
52.488 Million cell updates/sec

Title: US-09-879-257A-3
Perfect score: 27
Sequence: 1 LVGDIGNVNMDFVLSPEINTIYLGG 27

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 4 seqs, 1944 residues

Word size : 6

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: listing first 45 summaries

Database : rag6.pep:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description

No matches found

Search completed: December 16, 2004, 07:43:29
Job time : 0.001 secs

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OM protein - protein search, using sw model

Run on: December 16, 2004, 07:46:14 ; Search time 0.090604 Seconds
(without alignments)
0.145 Million cell updates/sec

Title: US-09-879-257A-3

Perfect score: 27

Sequence: 1 LVGDIGNVMWDFVLSPEINTIYLGG 27

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1 seqs, 486 residues

Word size : 6

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : rapb6.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query			
No.	Score	Match	Length	ID
Description				

No matches found

Search completed: December 16, 2004, 07:46:15
Job time : 0.090604 secs

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OM protein - protein search, using sw model

Run on: December 16, 2004, 07:47:32 ; Search time 0.001 Seconds
(without alignments)
26.244 Million cell updates/sec

Title: US-09-879-257A-3

Perfect score: 27
Sequence: 1 LVGDIGNVMWDFVLSPDEINTIYLGG 27

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2 seqs, 972 residues

Word size : 6

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : rapm6.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match	Length	ID	Description

No matches found

Search completed: December 16, 2004, 07:47:32
Job time : 0.001 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 16, 2004, 07:48:45 ; Search time 0.001 Seconds
(without alignments)
13.122 Million cell updates/sec

Title: US-09-879-257A-3
Perfect score: 27
Sequence: 1 LVGDIGNVMWDFVLSPEINTIYLG 27

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1 seqs, 486 residues

Word size : 6

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : rpr6.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description

No matches found					

Search completed: December 16, 2004, 07:48:46
Job time : 1 secs

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OM protein - protein search, using sw model

Run on: December 16, 2004, 07:43:29 ; Search time 0.001 Seconds
(without alignments)
23.328 Million cell updates/sec

Title: US-09-879-257A-46
Perfect score: 12
Sequence: 1 DPRVRGLYFPAG 12

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 4 seqs, 1944 residues

Word size : 6

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : rag6.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description

No matches found

Search completed: December 16, 2004, 07:43:29
Job time : 0.001 secs

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OM protein - protein search, using sw model

Run on: December 16, 2004, 07:46:14 : Search time 0.0402685 Seconds
(without alignments)
0.145 Million cell updates/sec

Title: US-09-879-257A-46
Perfect score: 12
Sequence: 1 DPRVRLGLFPAG 12

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1 seqs, 486 residues

Word size : 6

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : rapb6.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	ID	Description
No.	Score	Match	Length

No matches found

Search completed: December 16, 2004, 07:46:15
Job time : 0.0402685 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 16, 2004, 07:47:32 : Search time 0.001 Seconds
(without alignments)
11.664 Million cell updates/sec

Title: US-09-879-257a-46
Perfect score: 12
Sequence: 1 DPRVRLGLYFPAG 12

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2 seqs, 972 residues

Word size : 6

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : rapm6.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match	Length	ID	Description

No matches found

Search completed: December 16, 2004, 07:47:32
Job time : 0.001 secs

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OM protein - protein search, using sw model

Run on: December 16, 2004, 07:48:45 ; Search time 0.001 seconds
(without alignments)
5.832 Million cell updates/sec

Title: US-09-879-257A-46
Perfect score: 12
Sequence: 1 DPRVRGLYFPAG 12

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1 seqs, 486 residues

Word size : 6

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : rpr6.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description

No matches found					

Search completed: December 16, 2004, 07:48:46
Job time : 0.001 secs

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OM protein - protein search, using sw model

Run on: December 16, 2004, 07:43:29 ; Search time 0.001 Seconds
(without alignments)
23.328 Million cell updates/sec

Title: US-09-879-257A-4
Perfect score: 12
Sequence: 1 LKKGYTVGAEAS 12

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 4 seqs, 1944 residues

Word size : 6

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : rag6.ped:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match	Length	ID	Description

No matches found

Search completed: December 16, 2004, 07:43:29
Job time : 0.001 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 16, 2004, 07:46:14 ; Search time 0.0402685 Seconds
(without alignments)
0.145 Million cell updates/sec

Title: US-09-879-257A-4
Perfect score: 12
Sequence: 1 LKGYTVGAFAAS 12

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1 seqs, 486 residues

Word size : 6

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 45 summaries

Database : rapb6.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description

No matches found					

Search completed: December 16, 2004, 07:46:15
Job time : 0.0402685 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 16, 2004, 07:47:32 ; Search time 0.001 seconds
(without alignments)
11.664 Million cell updates/sec

Title: US-09-879-257A-4
Perfect score: 12
Sequence: 1 LKKGYTVGAENS 12

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2 seqs, 972 residues

Word size : 6

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : rapm6.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match	Length	ID	Description
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No matches found

Search completed: December 16, 2004, 07:47:32
Job time : 0.001 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 16, 2004, 07:48:45 : Search time 0.001 Seconds
(without alignments)
5.832 Million cell updates/sec

Title: US-09-879-257A-4
Perfect score: 12
Sequence: 1 LKKGYTVGAERAS 12

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1 seqs, 486 residues

Word size : 6

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 45 summaries

Database : rpr6.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	ID	Description

No matches found			

Search completed: December 16, 2004, 07:48:46
Job time : 0.001 secs

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OM protein - protein search, using sw model

Run on: December 16, 2004, 07:43:29 ; Search time 0.001 Seconds
(without alignments)
29.160 Million cell updates/sec

Title: US-09-879-257A-50
Perfect score: 15
Sequence: 1 ERVEWLRKQLQDVHN 15

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 4 seqs, 1944 residues

Word size : 6

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : rag6.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query				
No.	Score	Match	Length	ID	Description

No matches found

Search completed: December 16, 2004, 07:43:29
Job time : 0.001 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 16, 2004, 07:46:14 ; Search time 0.0503356 Seconds
(without alignments)
0.145 Million cell updates/sec

Title: US-09-879-257a-50
Perfect score: 15
Sequence: 1 ERVWMLRKXIQDVHN 15

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1 seqs, 486 residues

Word size : 6

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : rapb6.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match	Length	ID	Description

No matches found

Search completed: December 16, 2004, 07:46:15
Job time : 0.0503356 secs

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OM protein - protein search, using sw model

Run on: December 16, 2004, 07:47:32 ; Search time 0.001 Seconds
(without alignments)
14.580 Million cell updates/sec

Title: US-09-879-257a-50
Perfect score: 15
Sequence: 1 ERVWMLKKLQDVHN 15

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2 seqs, 972 residues

Word size : 6

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : rapm6.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description

No matches found

Search completed: December 16, 2004, 07:47:32
Job time : 0.001 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 16, 2004, 07:48:45 ; Search time 0.001 Seconds
(without alignments)
7.290 Million cell updates/sec

Title: US-09-879-257A-50
Perfect score: 15
Sequence: 1 ERVEMLRKXLDVHN 15

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1 seqs, 486 residues

Word size : 6

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : rpr6.pdb:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match	Length	ID	Description
No matches found					

Search completed: December 16, 2004, 07:48:46
Job time : 0.001 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 16, 2004, 07:43:29 : Search time 0.001 Seconds
(without alignments)
19.440 Million cell updates/sec

Title: US-09-879-257A-5
Perfect score: 10
Sequence: 1 RALKYVQGE 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 4 seqs, 1944 residues

Word size : 6

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : rag6.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description

No matches found					

Search completed: December 16, 2004, 07:43:29
Job time : 0.001 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 16, 2004, 07:46:14 ; Search time 0.033557 Seconds
(without alignments)
0.145 Million cell updates/sec

Title: US-09-879-257A-5
Perfect score: 10
Sequence: 1 RALKVEYQGE 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1 seqs, 486 residues

Word size : 6

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : rapb6.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description

No matches found

Search completed: December 16, 2004, 07:46:15
Job time : 0.033557 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 16, 2004, 07:47:32 ; Search time 0.001 Seconds
(without alignments)
9.720 Million cell updates/sec

Title: US-09-879-257A-5
Perfect score: 10
Sequence: 1 RALKYEVQGE 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2 seqs, 972 residues

Word size : 6

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : rapm6.pap:*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match	Length	ID	Description
No matches found					

Search completed: December 16, 2004, 07:47:32
Job time : 0.001 secs

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OM protein - protein search, using sw model

Run on: December 16, 2004, 07:48:45 ; Search time 0.001 Seconds
(without alignments)
4.860 Million cell updates/sec

Title: US-09-879-257A-5
Perfect score: 10
Sequence: 1 RALKYEVQGE 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1 seqe, 486 residues

Word size : 6

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : rpr6.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match	Length	ID	Description

No matches found

Search completed: December 16, 2004, 07:48:46
Job time : 0.001 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2004, 09:44:28 ; Search time 50 Seconds
(without alignments)
389.950 Million cell updates/sec

Title: US-09-879-257A-6_COPY_1_294
Perfect score: 1516
Sequence: 1 MVSEIKTLVFPFGTGLAK.....IYDAEYVKYFVRAQYAGD 294

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 65000 summaries

Database : Issued Patente AA: *
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep: *
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query			
No.	Score	Match	Length	ID
Description				

No matches found

Search completed: December 14, 2004, 09:55:15
Job time : 53 secs

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OM protein - protein search, using sw model

Run on: December 14, 2004, 09:53:34 ; Search time 164 Seconds
(without alignments)
640.307 Million cell updates/sec

Title: US-09-879-257A-6_COPY_1_294
Sequence: 1 MVSSEIKTLVTFPGGTGDLAK.....IYDEAEVKKYFVRAQYGAGD 294

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1585576 seqs, 357178320 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 65000 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubppa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubppa/PC7_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubppa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubppa/PC7US_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubppa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubppa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubppa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubppa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubppa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubppa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubppa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubppa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1516	100.0	486 9 US-09-879-257A-6	Sequence 6, Appl1

ALIGNMENTS

RESULT 1
US-09-879-257A-6
; Sequence 6, Application US/09879257A
; Patent No. US20020081650A1
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, SACHIKO
; APPLICANT: HANADA, TOSHIRO

; APPLICANT: SHIRO, MINORU
; APPLICANT: KOBATAKE, SHINZO
; TITLE OF INVENTION: HYBRID ENZYMES AND USE THEREOF
; FILE REFERENCE: 55986(70281)
; CURRENT APPLICATION NUMBER: US/09/879,257A
; CURRENT FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 486
; TYPE: PRT
; ORGANISM: Leuconostoc mesenteroides
US-09-879-257A-6

Query Match 100.0%; Score 1516; DB 9; Length 486;
Best Local Similarity 100.0%; Pred. No. 6.4e-127;
Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MVSSEIKTLVTFPGGTGDLAKRLYPVFNLYKKGYLQKHFALVGTARQALNDSFKQLVR	60
DB	1	MVSSEIKTLVTFPGGTGDLAKRLYPVFNLYKKGYLQKHFALVGTARQALNDSFKQLVR	60
QY	61	DSIKDFTDDQAQAEAFIEHFSYRAHDVTDAASTAVLKEAIEBAADKFDIDGNRIFYNSVA	120
DB	61	DSIKDFTDDQAQAEAFIEHFSYRAHDVTDAASTAVLKEAIEBAADKFDIDGNRIFYNSVA	120
QY	121	PRFPGTIAKYLKSGGLADTGYNRLMTEKPGTSYDTAAELQNDLENAFDNQLFRIDHY	180
DB	121	PRFPGTIAKYLKSGGLADTGYNRLMTEKPGTSYDTAAELQNDLENAFDNQLFRIDHY	180
QY	181	LGEKMNQNIALLRGNPIFDAAMNKDYIKNVQVTLSEVLGVEERAGYDTAGALLDMIQN	240
DB	181	LGEKMNQNIALLRGNPIFDAAMNKDYIKNVQVTLSEVLGVEERAGYDTAGALLDMIQN	240
QY	241	HTMQIVGMLAMEKPESTTDKDIRAKNAAFNALKIYDEAEVKKYFVRAQYGAGD	294
DB	241	HTMQIVGMLAMEKPESTTDKDIRAKNAAFNALKIYDEAEVKKYFVRAQYGAGD	294

Search completed: December 14, 2004, 10:06:55
Job time : 166 secs

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OM protein - protein search, using sw model

Run on: December 14, 2004, 09:47:04 : Search time 488 Seconds
(without alignments)
667.524 Million cell updates/sec

Title: US-09-879-257a-6_COPY_1_294
Perfect score: 1516
Sequence: 1 MVSIRKTLVTFPGGTGLAK.....IYDAEVNKYFVRQYAGD 294

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 6730630 seqs, 1107998698 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 65000 summaries

Database : Pending Patents AA Main:*

1: /cgn2_6/ptodata/1/paa/PCRTUS_COMB.pep:*
2: /cgn2_6/ptodata/1/paa/US06_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/US07_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US08_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US081_COMB.pep:*
6: /cgn2_6/ptodata/1/paa/US082_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US083_COMB.pep:*
8: /cgn2_6/ptodata/1/paa/US084_COMB.pep:*
9: /cgn2_6/ptodata/1/paa/US085_COMB.pep:*
10: /cgn2_6/ptodata/1/paa/US086_COMB.pep:*
11: /cgn2_6/ptodata/1/paa/US087_COMB.pep:*
12: /cgn2_6/ptodata/1/paa/US088_COMB.pep:*
13: /cgn2_6/ptodata/1/paa/US089_COMB.pep:*
14: /cgn2_6/ptodata/1/paa/US090_COMB.pep:*
15: /cgn2_6/ptodata/1/paa/US091_COMB.pep:*
16: /cgn2_6/ptodata/1/paa/US092_COMB.pep:*
17: /cgn2_6/ptodata/1/paa/US093_COMB.pep:*
18: /cgn2_6/ptodata/1/paa/US094_COMB.pep:*
19: /cgn2_6/ptodata/1/paa/US095_COMB.pep:*
20: /cgn2_6/ptodata/1/paa/US096_COMB.pep:*
21: /cgn2_6/ptodata/1/paa/US097A_COMB.pep:*
22: /cgn2_6/ptodata/1/paa/US097B_COMB.pep:*
23: /cgn2_6/ptodata/1/paa/US098_COMB.pep:*
24: /cgn2_6/ptodata/1/paa/US099A_COMB.pep:*
25: /cgn2_6/ptodata/1/paa/US099B_COMB.pep:*
26: /cgn2_6/ptodata/1/paa/US100_COMB.pep:*
27: /cgn2_6/ptodata/1/paa/US101_COMB.pep:*
28: /cgn2_6/ptodata/1/paa/US102_COMB.pep:*
29: /cgn2_6/ptodata/1/paa/US103_COMB.pep:*
30: /cgn2_6/ptodata/1/paa/US104_COMB.pep:*
31: /cgn2_6/ptodata/1/paa/US105_COMB.pep:*
32: /cgn2_6/ptodata/1/paa/US106_COMB.pep:*
33: /cgn2_6/ptodata/1/paa/US107_COMB.pep:*
34: /cgn2_6/ptodata/1/paa/US108_COMB.pep:*
35: /cgn2_6/ptodata/1/paa/US109_COMB.pep:*
36: /cgn2_6/ptodata/1/paa/US60_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

#

Result No.	Score	Query Match	Length DB	ID	Description
1	1516	100.0	486	22	US-09-791-537-11271, A
2	1516	100.0	486	23	US-09-879-257a-6 Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-09-791-537-11271
; Sequence 11271, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11271
; LENGTH: 486
; TYPE: PRT
; ORGANISM: Leuconostoc mesenteroides
US-09-791-537-11271

Query Match
Best Local Similarity 100.0%; Score 1516; DB 22; Length 486;
Pred. No. 5 5e-145;
Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MVSIRKTLVTFPGGTGLAKRKLPSYFNLYKKGYLQGFALVGTARQALNDFKQLVR	60
DB	1	MVSIRKTLVTFPGGTGLAKRKLPSYFNLYKKGYLQGFALVGTARQALNDFKQLVR	60
QY	61	DSIDFTDDQAQAFAIEHPSYRAHDVTDAASVAVLKEATLEADKPDIDNRIFYMSVA	120
DB	61	DSIDFTDDQAQAFAIEHPSYRAHDVTDAASVAVLKEATLEADKPDIDNRIFYMSVA	120
QY	121	PRFPGTIAKYLKSEGLADTGYNRLMTEKPGTSYDTAAELQNDLENAFDNDQFRIDHY	180
DB	121	PRFPGTIAKYLKSEGLADTGYNRLMTEKPGTSYDTAAELQNDLENAFDNDQFRIDHY	180
QY	181	LGEKMNQNIARLRFNFIPTAAMNKDYIKNVQVTLSEVLGYEBRAGYYDTAGALLDMION	240
DB	181	LGEKMNQNIARLRFNFIPTAAMNKDYIKNVQVTLSEVLGYEBRAGYYDTAGALLDMION	240
QY	241	HTMIVGWLMEKESEFTDDIRAAKNAAFYALKIYDEAEVNNKFVRAQYAGD	294
DB	241	HTMIVGWLMEKESEFTDDIRAAKNAAFYALKIYDEAEVNNKFVRAQYAGD	294

RESULT 2
US-09-879-257a-6
; Sequence 6, Application US/09879257A
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, SACHIRO
; APPLICANT: HANADA, TOSHIRO
; APPLICANT: SHIRO, MINORU
; APPLICANT: KOBATAKE, SHINZO
; TITLE OF INVENTION: HYBRID ENZYMES AND USE THEREOF
; FILE REFERENCE: 55986(70281)
; CURRENT APPLICATION NUMBER: US/09/879,257A
; CURRENT FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 486
; TYPE: PRT
; ORGANISM: Leuconostoc mesenteroides

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OM protein - protein search, using sw model

Run on: December 14, 2004, 09:50:04 ; Search time 29 Seconds

(without alignments)
434.426 Million cell updates/sec

Title: US-09-879-257a-6_COPY_1_294
Perfect score: 1516
Sequence: 1 MVSEIKTLVFPFGSTGLAK.....IYDEAEVNVKVFVRAGAGD 294

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 16218 seqs, 42851568 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 65000 summaries

Database : Pending Patents AA New:*

- 1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*
- 2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
- 3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
- 4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
- 5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
- 6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
- 7: /cgn2_6/ptodata/1/paa/US11_NEW_COMB.pep:*
- 8: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description

No matches found

Search completed: December 14, 2004, 10:04:05
Job time : 32 secs

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OM protein - protein search, using sw model

Run on: December 14, 2004, 09:43:43 ; Search time 45 Seconds
(without alignments)
628.616 Million cell updates/sec

Title: US-09-879-257a-6_COPY_1_294
Perfect score: 1516
Sequence: 1 MVSEIKTLVTFPGGTGDLAKR.....IYDEAEVVKYFVRAQYGAGD 294

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 65000 summaries

Database : PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1516	100.0	486	1 A39864	glucose-6-phosphat

ALIGNMENTS

RESULT 1
A39864
glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) - leuconostoc mesenteroides
C/Species: Leuconostoc mesenteroides
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C/Accession: A39864; A29027
R/Lee, W.T.; Flynn, T.G.; Lyons, C.; Levy, H.R.
J. Biol. Chem. 266, 13028-13034, 1991
A/Title: Cloning of the gene and amino acid sequence for glucose 6-phosphate dehydrogenase
A/Reference number: A39864; MUID:91302321; PMID:2071589
A/Accession: A39864
A/Molecule type: DNA
A/Residues: 1-486 <LBS>
A/Cross-references: UNIPROT:P11411; GB:M64446; NID:G149630; PTDN:AAA25265.1; PID:G149631
R/Bhadbhade, M.M.; Adams, M.J.; Flynn, T.G.; Levy, H.R.
FEBS Lett. 211, 243-246, 1987
A/Title: Sequence identity between a lysine-containing peptide from leuconostoc mesenteroides
A/Reference number: A29027; MUID:87105980; PMID:3100332
A/Accession: A29027
A/Molecule type: Protein
A/Residues: 147-153, 'H', 155, 'I', 157-164, 'F', 166-188 <BHA>
C/Superfamily: glucose-6-phosphate dehydrogenase

C/Keywords: oxidoreductase; pentose phosphate pathway

Query Match 100.0%; Score 1516; DB 1; Length 486;
Best Local Similarity 100.0%; Pred. No. 1.5e-100;
Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MVSEIKTLVTFPGGTGDLAKRKLPSVFNLYKKGYLQKHFAIVGTARQALNDDEFFKQLYR	60
Db	1	MVSEIKTLVTFPGGTGDLAKRKLPSVFNLYKKGYLQKHFAIVGTARQALNDDEFFKQLYR	60
Qy	61	DSIKDFTDDQQAQAEAFIEHESYRAHDVTDAAASYVLKEAIEBAADKPDIDGNRIFYMSVA	120
Db	61	DSIKDFTDDQQAQAEAFIEHESYRAHDVTDAAASYVLKEAIEBAADKPDIDGNRIFYMSVA	120
Qy	121	PRFPGTIATKYIKSGGLADTGYNRLMEKPGTSYDTPAAELQNDLENAFPDNOLEFRIDHY	180
Db	121	PRFPGTIATKYIKSGGLADTGYNRLMEKPGTSYDTPAAELQNDLENAFPDNOLEFRIDHY	180
Qy	181	LGEKEMVONIALRFGNPIFDAAMNKDYIKNVQVTLSEVLGVEERAGYVDTAGALLDMION	240
Db	181	LGEKEMVONIALRFGNPIFDAAMNKDYIKNVQVTLSEVLGVEERAGYVDTAGALLDMION	240
Qy	241	HTMQIVGWLAMEKESFTDKDIRAAKNAAFNALKIYDEAEVVKYFVRAQYGAGD	294
Db	241	HTMQIVGWLAMEKESFTDKDIRAAKNAAFNALKIYDEAEVVKYFVRAQYGAGD	294

Search completed: December 14, 2004, 09:54:19
Job time : 48 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2004, 09:43:03 ; Search time 206 Seconds
(without alignments)
821.166 Million cell updates/sec

Title: US-09-879-257A-6_COPY_1_294
Perfect score: 1516
Sequence: 1 MVSRIKTLVTFPGGTGLAK.....IYDEAEVVKYFVRAGYGAQD 294

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 65000 summaries

Database : UniProt 02:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	ID	Description

No matches found

Search completed: December 14, 2004, 09:53:27
Job time : 209 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: December 14, 2004, 09:39:47, Search time 171 Seconds
(without alignments)
616.763 Million cell updates/sec

Title: US-09-879-257a-6_COPY_1_294
Perfect score: 1516
Sequence: 1 MWSIKITLVTFPGGTGLAK.....IYDAEVNKFVRQYAGD 294

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 65000 summaries

Database: 1: Geneseqp23Sep04:*
2: geneseqp1980s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1516	100.0	486	4 AAB74045	AAB74045 L. pseudo
2	1516	100.0	486	4 AAB74044	AAB74044 L. pseudo
3	1516	100.0	486	4 AAB74041	AAB74041 Leuconost
4	1516	100.0	486	5 AAB21112	AAB21112 Leuconost

ALIGNMENTS

RESULT 1
AAB74045
ID AAB74045 standard; protein; 486 AA.
XX
AC AAB74045;
XX
DT 15-JUN-2001 (first entry)
XX
L. pseudomesenteroides glucose-6-phosphate dehydrogenase mutant #4.
XX
DE Glucose-6-phosphate dehydrogenase; site-directed mutagenesis;
KM enzyme stability; mutant; mutein.
XX
OS Leuconostoc pseudomesenteroides.
XX
XX Synthetic.

PH Key Location/Qualifiers
FT Misc-difference 337
XX /note= "wild-type Ser substituted by Ala"
XX
XX JP2001037480-A.
XX
XX 13-FEB-2001.
XX
XX 28-JUL-1999; 99JP-00213427.
XX
XX 28-JUL-1999; 99JP-00213427.
XX
XX (TOMO) TOYOBO KK.
XX
XX WPI; 2001-285598/30.
XX
XX

Mutant glucose-6-phosphate dehydrogenase and its preparation.

Example 1; Page; 15pp; Japanese.

CC The present sequence is one of nine mutants of the glucose-6-phosphate
CC dehydrogenase from Leuconostoc pseudomesenteroides which were synthesized
CC by site-directed mutagenesis. Primers were used to mutate the sequence of
CC the wild-type glucose-6-phosphate dehydrogenase gene within the
CC recombinant plasmid pG6D66 to produce plasmids pG6D66M1 and pG6D66M9. The
CC present sequence is encoded by recombinant plasmid pG6D66M4. The
CC stability of the mutant enzymes in liquid state is improved compared to
CC of a mutant glucose-6-phosphate dehydrogenase of high purity in large
CC quantities. Note: The present sequence is not shown in the specification
CC but is derived from the Leuconostoc pseudomesenteroides wild-type glucose
CC -6-phosphate dehydrogenase sequence shown in AAB74041
XX
XX

Sequence 486 AA;

Query Match 100.0%; Score 1516; DB 4; Length 486;
Best Local Similarity 100.0%; Pred. No. 7.7e-131;
Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MWSIKITLVTFPGGTGLAKRKLPSVFNLYKKGYLQKHFAIVGTARQLNDDFKQLVR	60
DB	1	MWSIKITLVTFPGGTGLAKRKLPSVFNLYKKGYLQKHFAIVGTARQLNDDFKQLVR	60
QY	61	DSIKRPTDDQAQAEFIEHFSYRAVDYDAASYAVLTKERIEBAAXPDIDGNRIPTMSYA	120
DB	61	DSIKRPTDDQAQAEFIEHFSYRAVDYDAASYAVLTKERIEBAAXPDIDGNRIPTMSYA	120
QY	121	PRPFGTIKYLKSEGLADVTGNRLMIEKPFSTSYDTAAELQNDLENAPDDNQLEFRIDHY	180
DB	121	PRPFGTIKYLKSEGLADVTGNRLMIEKPFSTSYDTAAELQNDLENAPDDNQLEFRIDHY	180
QY	181	LGEKENVONIAALRFGNPIEDAAWNRDYLKNVQVTLSEVLGVERAGYVDTAGALLDMION	240
DB	181	LGEKENVONIAALRFGNPIEDAAWNRDYLKNVQVTLSEVLGVERAGYVDTAGALLDMION	240
QY	241	HTMOIVGWLAMEKPESTFDKDIRAARNAAFNAKLYDEEVNKFVRQYAGD	294
DB	241	HTMOIVGWLAMEKPESTFDKDIRAARNAAFNAKLYDEEVNKFVRQYAGD	294

RESULT 2
AAB74044
ID AAB74044 standard; protein; 486 AA.
XX
AC AAB74044;
XX
DT 15-JUN-2001 (first entry)
XX
L. pseudomesenteroides glucose-6-phosphate dehydrogenase mutant #3.
XX
DE Glucose-6-phosphate dehydrogenase; site-directed mutagenesis;
KM enzyme stability; mutant; mutein.
XX
XX

OS Leuconostoc pseudomesenteroides.
OS Synthetic.

Key Location/Qualifiers
FT Misc-difference 324
PT /note= "Wild-type Asp substituted by Gly"

XX JP2001037480-A.

XX 13-FEB-2001.

XX 28-JUL-1999; 99JP-00213427.

XX 28-JUL-1999; 99JP-00213427.

XX (TOYO) TOYOBO KK.

XX WPI; 2001-285598/30.

XX Mutant glucose-6-phosphate dehydrogenase and its preparation.

XX Example 1; Page: 15pp; Japanese.

CC The present sequence is one of nine mutants of the glucose-6-phosphate
CC dehydrogenase from Leuconostoc pseudomesenteroides which were synthesised
CC by site-directed mutagenesis. Primers were used to mutate the sequence of
CC the wild-type glucose-6-phosphate dehydrogenase gene within the
CC recombinant plasmid pG6D6 to produce plasmids pG6D6M1 and pG6D6M9. The
CC present sequence is encoded by recombinant plasmid pG6D6M3. The
CC stability of the mutant enzymes in liquid state is improved compared to
CC the wild-type enzyme. The disclosed method is useful for the preparation
CC of a mutant glucose-6-phosphate dehydrogenase of high purity in large
CC quantities. Note: The present sequence is not shown in the specification
CC but is derived from the Leuconostoc pseudomesenteroides wild-type glucose
CC -6-phosphate dehydrogenase sequence shown in AAB74041

XX SQ Sequence 486 AA;

Query Match 100.0%; Score 1516; DB 4; Length 486;

Best Local Similarity 100.0%; Pred. No. 7,7e-131; Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWSSEIKTLVTFPGGTGDLAKRKLYPSVFNLYKKGYLQKHFAIVGTARQALNDEPFQVLR 60
DB 1 MWSSEIKTLVTFPGGTGDLAKRKLYPSVFNLYKKGYLQKHFAIVGTARQALNDEPFQVLR 60
QY 61 DSIKPFTDQAQAFAEIEHFSYRAHDVTDAAAYAVLKEAIEBAADFPDIDGNRIFYMSVA 120
DB 61 DSIKPFTDQAQAFAEIEHFSYRAHDVTDAAAYAVLKEAIEBAADFPDIDGNRIFYMSVA 120
QY 121 PRFFGTIAKYLSEGLADTYGNRLMIERPGTSYDTAAELQNDLENAPDDNQLPRIDHY 180
DB 121 PRFFGTIAKYLSEGLADTYGNRLMIERPGTSYDTAAELQNDLENAPDDNQLPRIDHY 180
QY 181 LGEKEMVQNIATLRFGNPIFDAAMNKQYIKNVQVTLSEVLGVEERAGYDTAGALLDMION 240
DB 181 LGEKEMVQNIATLRFGNPIFDAAMNKQYIKNVQVTLSEVLGVEERAGYDTAGALLDMION 240
QY 241 HTMOIVGWLAMEKPSFTDKDIRAANKAAFNALKIYDEAVNKYFVRAQYGAGD 294
DB 241 HTMOIVGWLAMEKPSFTDKDIRAANKAAFNALKIYDEAVNKYFVRAQYGAGD 294

RESULT 3
AAB74041

ID AAB74041 standard; protein; 486 AA.

XX AAB74041;

XX 15-JUN-2001 (first entry)

DB Leuconostoc pseudomesenteroides glucose-6-phosphate dehydrogenase.

KW Glucose-6-phosphate dehydrogenase; site-directed mutagenesis; mutant;
KW enzyme stability.

OS Leuconostoc pseudomesenteroides.

XX JP2001037480-A.

XX 13-FEB-2001.

XX 28-JUL-1999; 99JP-00213427.

XX 28-JUL-1999; 99JP-00213427.

XX (TOYO) TOYOBO KK.

XX WPI; 2001-285598/30.

XX N-PSDB; AAF82304.

XX Mutant glucose-6-phosphate dehydrogenase and its preparation.

XX Claim 3; Page 9-10; 15pp; Japanese.

CC The present sequence is glucose-6-phosphate dehydrogenase from
CC Leuconostoc pseudomesenteroides. Site-directed mutagenesis was used to
CC mutate the sequence of the wild-type glucose-6-phosphate dehydrogenase
CC gene within the recombinant plasmid pG6D6. The resulting plasmids,
CC pG6D6M1 to pG6D6M9, encode mutant glucose-6-phosphate dehydrogenase
CC enzymes. The invention relates to mutant glucose-6-phosphate
CC dehydrogenase enzymes in which at least one amino acid is added, deleted,
CC inserted or replaced, and the stability in liquid state is improved
CC compared to the wild type enzyme. The disclosed method is useful for the
CC preparation of a mutant glucose-6-phosphate dehydrogenase of high purity
CC in large quantities

XX SQ Sequence 486 AA;

Query Match 100.0%; Score 1516; DB 4; Length 486;

Best Local Similarity 100.0%; Pred. No. 7,7e-131; Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWSSEIKTLVTFPGGTGDLAKRKLYPSVFNLYKKGYLQKHFAIVGTARQALNDEPFQVLR 60
DB 1 MWSSEIKTLVTFPGGTGDLAKRKLYPSVFNLYKKGYLQKHFAIVGTARQALNDEPFQVLR 60
QY 61 DSIKPFTDQAQAFAEIEHFSYRAHDVTDAAAYAVLKEAIEBAADFPDIDGNRIFYMSVA 120
DB 61 DSIKPFTDQAQAFAEIEHFSYRAHDVTDAAAYAVLKEAIEBAADFPDIDGNRIFYMSVA 120
QY 121 PRFFGTIAKYLSEGLADTYGNRLMIERPGTSYDTAAELQNDLENAPDDNQLPRIDHY 180
DB 121 PRFFGTIAKYLSEGLADTYGNRLMIERPGTSYDTAAELQNDLENAPDDNQLPRIDHY 180
QY 181 LGEKEMVQNIATLRFGNPIFDAAMNKQYIKNVQVTLSEVLGVEERAGYDTAGALLDMION 240
DB 181 LGEKEMVQNIATLRFGNPIFDAAMNKQYIKNVQVTLSEVLGVEERAGYDTAGALLDMION 240
QY 241 HTMOIVGWLAMEKPSFTDKDIRAANKAAFNALKIYDEAVNKYFVRAQYGAGD 294
DB 241 HTMOIVGWLAMEKPSFTDKDIRAANKAAFNALKIYDEAVNKYFVRAQYGAGD 294

RESULT 4
AAE21112

ID AAE21112 standard; protein; 486 AA.

XX AAE21112;

XX 01-JUL-2002 (first entry)

DB Leuconostoc mesenteroides glucose-6-phosphate dehydrogenase (G6PDH).

KW C-reactive protein; CRP, hybrid enzyme; G6PDH; macromolecule measurement;
KW quantitative analysis; qualitative; glucose-6-phosphate dehydrogenase.

XX Leuconostoc mesenteroides.
 OS
 XX EPI182213-A1.
 FN
 XX 27-FEB-2002.
 PD
 XX 08-JUN-2001; 2001EP-00113996.
 PF
 XX 12-JUN-2000; 2000JP-00174604.
 PR
 XX 11-SEP-2000; 2000JP-00274219.
 XX
 PA (WAKP) WAKO PURE CHEM IND LTD.
 XX
 PI Yamamoto S, Shiro M, Hanada T, Kobatake S;
 XX
 DR WPI; 2002-294073/34.
 XX
 PT Hybrid enzyme having a foreign peptide, useful for measuring
 PT macromolecule material in homogeneous system, has its activity modulated
 PT when a material capable of binding the peptide is introduced.
 XX
 PS Claim 17; Page 25-28; 74pp; English.
 XX
 CC The invention relates to a hybrid enzyme having a foreign peptide. The
 CC hybrid enzyme has an enzyme activity similar to that prior to the
 CC substitution or insertion of the peptide and having a property that the
 CC hybrid enzyme activity is modulated or modified when a material having
 CC binding ability to the peptide introduced by substitution or insertion is
 CC bound to the peptide moiety. The hybrid enzyme is useful for measuring C-
 CC reactive protein (CRP) by using an anti-CRP antibody in combination, and
 CC for measurement of a material containing the peptide introduced into the
 CC hybrid enzyme, or a material having binding ability to the peptide
 CC introduced into the hybrid enzyme. A recombinant DNA is useful for
 CC producing a protein having enzyme activity of G6PD, beta-galactosidase or
 CC alkaline phosphatase and a property that the enzyme is modulated when a
 CC material having binding ability to an amino acid sequence introduced into
 CC the enzyme by substitution or insertion is bound to the amino acid
 CC sequence, by culturing the transformant and collecting the protein. The
 CC hybrid enzyme is useful for both qualitative and quantitative analysis.
 CC The present sequence is Leuconostoc mesenteroides glucose-6-phosphate
 CC dehydrogenase (G6PDH) used in the invention
 XX
 XX Sequence 486 AA;
 SQ
 Query Match 100.0%; Score 1516; DB 5; Length 486;
 Best Local Similarity 100.0%; Pred. No. 7.7e-131;
 Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MVSSEIKTLVTFPGGTGDLAKRKLTPSVNLYKGYLQGHFAIVGTARQALNDDERKQLYR 60
 DB 1 MVSSEIKTLVTFPGGTGDLAKRKLTPSVNLYKGYLQGHFAIVGTARQALNDDERKQLYR 60
 QY 61 DSIDKFTDDQAQAEAFIEHFSYRAHDVTDAAASYAVLKEAIEBAADKPDIDGNRIIFYMSVA 120
 DB 61 DSIDKFTDDQAQAEAFIEHFSYRAHDVTDAAASYAVLKEAIEBAADKPDIDGNRIIFYMSVA 120
 QY 121 PRFFGTIAKYLKSEGLADTGVNRLMEKPFSTSYDTAAELQNDLENAFDDNQLEFRIDHY 180
 DB 121 PRFFGTIAKYLKSEGLADTGVNRLMEKPFSTSYDTAAELQNDLENAFDDNQLEFRIDHY 180
 QY 181 LGKEMVQNIALLRGNPIFDAAMNDYIKNOVTLSEVLGYEERAGYDTAGALLDMTON 240
 DB 181 LGKEMVQNIALLRGNPIFDAAMNDYIKNOVTLSEVLGYEERAGYDTAGALLDMTON 240
 QY 241 HTMOIVGWLAMEKPESTDKDIRAKNAAFNALKIYDEAEVVKYFVRAQYGAGD 294
 DB 241 HTMOIVGWLAMEKPESTDKDIRAKNAAFNALKIYDEAEVVKYFVRAQYGAGD 294